



**FIGURE 22.10.** Using genetic divergence to estimate when populations separated. At time  $T$ , two species separate from a single ancestral population, which had effective size  $N_e$ . (A) The time to common ancestry of two lineages sampled from different populations averages  $T + 2N_e$ . This is because, tracing backward in time, even when the ancestral lineages (A, B) enter the same population, it will still take  $\sim 2N_e$  generations for them to coalesce. When species are closely related ( $T$  less than  $\sim 2N_e$ ), it is likely that an ancestral lineage (C) will not coalesce within its own species during time  $T$ , and that the genealogy will not correspond to the species' phylogeny. In this example, C is more closely related to A than it is to B. (B) If speciation is not instantaneous, there will be a period  $T^*$  during which some genes can flow between species. If there happens to be no gene flow in the ancestry of a gene, genealogies are likely to coincide with the phylogeny, with relatively ancient divergence (i.e., before  $T + T^*$ ; A–E, which are a genealogy at one gene [red]). However, some loci will show gene flow and will have discordant genealogies (e.g., W–Y). V–Z are a genealogy at another gene (green).